

## RAW SEQUENCE LISTING

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Application Serial Number:

101540, 808

Source:

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7/6/05

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## RAW SEQUENCE LISTING

DATE: 07/06/2005

PATENT APPLICATION: US/10/540,808

TIME: 15:03:50

Input Set : A:\Sequence\_Listing.txt

Output Set: N:\CRF4\07062005\J540808.raw

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4 <110> APPLICANT: Muda, Marco
6 <120> TITLE OF INVENTION: Spliced Variants of LGR6
8 <130> FILE REFERENCE: 05558.0029.PCUS00
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/540,808
C--> 10 <141> CURRENT FILING DATE: 2005-06-27
10 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/051091
11 <151> PRIOR FILING DATE: 2003-12-23
13 <150> PRIOR APPLICATION NUMBER: US 60/436,001
14 <151> PRIOR FILING DATE: 2002-12-26
16 <160> NUMBER OF SEQ ID NOS: 6
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 3306
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (47)..(2791)
28 <223> OTHER INFORMATION:
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36 Pro Arg Leu Thr Leu Val Cys Gln Val Ser Ile Ile Ile Ser Ala Arg
37   5                10                15
39 gac ctc agc atg aac aac ctc aca gag ctt cag cct ggc ctc ttc cac      151
40 Asp Leu Ser Met Asn Asn Leu Thr Glu Leu Gln Pro Gly Leu Phe His
41 20                25                30                35
43 cac ctg cgc ttc ttg gag gag ctg cgt ctc tct ggg aac cat ctc tca      199
44 His Leu Arg Phe Leu Glu Glu Leu Arg Leu Ser Gly Asn His Leu Ser
45                40                45                50
47 cac atc cca gga caa gca ttc tct ggt ctc tac agc ctg aaa atc ctg      247
48 His Ile Pro Gly Gln Ala Phe Ser Gly Leu Tyr Ser Leu Lys Ile Leu
49                55                60                65
51 atg ctg cag aac aat cag ctg gga gga atc ccc gca gag gcg ctg tgg      295
52 Met Leu Gln Asn Asn Gln Leu Gly Gly Ile Pro Ala Glu Ala Leu Trp
53                70                75                80
55 gag ctg ccg agc ctg cag tcg ctg cgc cta gat gcc aac ctc atc tcc      343
56 Glu Leu Pro Ser Leu Gln Ser Leu Arg Leu Asp Ala Asn Leu Ile Ser
57                85                90                95
59 ctg gtc ccg gag agg agc ttt gag ggg ctg tcc tcc ctc cgc cac ctc      391
60 Leu Val Pro Glu Arg Ser Phe Glu Gly Leu Ser Ser Leu Arg His Leu

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64	Trp	Leu	Asp	Asp	Asn	Ala	Leu	Thr	Glu	Ile	Pro	Val	Arg	Ala	Leu	Asn	
65					120				125				130				
67	aac	ctc	cct	gcc	ctg	cag	gcc	atg	acc	ctg	gcc	ctc	aac	cgc	atc	agc	487
68	Asn	Leu	Pro	Ala	Leu	Gln	Ala	Met	Thr	Leu	Ala	Leu	Asn	Arg	Ile	Ser	
69				135				140				145					
71	cac	atc	ccc	gac	tac	gcg	ttc	cag	aat	ctc	acc	agc	ctt	gtg	gtg	ctg	535
72	His	Ile	Pro	Asp	Tyr	Ala	Phe	Gln	Asn	Leu	Thr	Ser	Leu	Val	Val	Leu	
73			150				155				160						
75	cat	ttg	cat	aac	aac	cgc	atc	cag	cat	ctg	ggg	acc	cac	agc	ttc	gag	583
76	His	Leu	His	Asn	Asn	Arg	Ile	Gln	His	Leu	Gly	Thr	His	Ser	Phe	Glu	
77		165				170				175							
79	ggg	ctg	cac	aat	ctg	gag	aca	cta	gac	ctg	aat	tat	aac	aag	ctg	cag	631
80	Gly	Leu	His	Asn	Leu	Glu	Thr	Leu	Asp	Leu	Asn	Tyr	Asn	Lys	Leu	Gln	
81	180				185				190				195				
83	gag	ttc	cct	gtg	gcc	atc	cgg	acc	ctg	ggc	aga	ctg	cag	gaa	ctg	ggg	679
84	Glu	Phe	Pro	Val	Ala	Ile	Arg	Thr	Leu	Gly	Arg	Leu	Gln	Glu	Leu	Gly	
85				200				205			210						
87	ttc	cat	aac	aac	aac	atc	aag	gcc	atc	cca	gaa	aag	gcc	ttc	atg	ggg	727
88	Phe	His	Asn	Asn	Asn	Ile	Lys	Ala	Ile	Pro	Glu	Lys	Ala	Phe	Met	Gly	
89			215				220			225							
91	aac	cct	ctg	cta	cag	acg	ata	cac	ttt	tat	gat	aac	cca	atc	cag	ttt	775
92	Asn	Pro	Leu	Leu	Gln	Thr	Ile	His	Phe	Tyr	Asp	Asn	Pro	Ile	Gln	Phe	
93			230				235			240							
95	gtg	gga	aga	tcg	gca	ttc	cag	tac	ctg	cct	aaa	ctc	cac	aca	cta	tct	823
96	Val	Gly	Arg	Ser	Ala	Phe	Gln	Tyr	Leu	Pro	Lys	Leu	His	Thr	Leu	Ser	
97		245				250			255								
99	ctg	aat	ggt	gcc	atg	gac	atc	cag	gag	ttt	cca	gat	ctc	aaa	ggc	acc	871
100	Leu	Asn	Gly	Ala	Met	Asp	Ile	Gln	Glu	Phe	Pro	Asp	Leu	Lys	Gly	Thr	
101	260				265				270				275				
103	acc	agc	ctg	gag	atc	ctg	acc	ctg	acc	cgc	gca	ggc	atc	cgg	ctg	ctc	919
104	Thr	Ser	Leu	Glu	Ile	Leu	Thr	Leu	Thr	Arg	Ala	Gly	Ile	Arg	Leu	Leu	
105				280				285			290						
107	cca	tcg	ggg	atg	tgc	caa	cag	ctg	ccc	agg	ctc	cga	gtc	ctg	gaa	ctg	967
108	Pro	Ser	Gly	Met	Cys	Gln	Gln	Leu	Pro	Arg	Leu	Arg	Val	Leu	Glu	Leu	
109			295				300			305							
111	tct	cac	aat	caa	att	gag	gag	ctg	ccc	agc	ctg	cac	agg	tgt	cag	aaa	1015
112	Ser	His	Asn	Gln	Ile	Glu	Glu	Leu	Pro	Ser	Leu	His	Arg	Cys	Gln	Lys	
113			310				315			320							
115	ttg	gag	gaa	atc	ggc	ctc	caa	cac	aac	cgc	atc	tgg	gaa	att	gga	gct	1063
116	Leu	Glu	Glu	Ile	Gly	Leu	Gln	His	Asn	Arg	Ile	Trp	Glu	Ile	Gly	Ala	
117		325				330			335								
119	gac	acc	ttc	agc	cag	ctg	agc	tcc	ctg	caa	gcc	ctg	gat	ctt	agc	tgg	1111
120	Asp	Thr	Phe	Ser	Gln	Leu	Ser	Ser	Leu	Gln	Ala	Leu	Asp	Leu	Ser	Trp	
121	340				345				350				355				
123	aac	gcc	atc	cgg	tcc	atc	cac	ccc	gag	gcc	ttc	tcc	acc	ctg	cac	tcc	1159
124	Asn	Ala	Ile	Arg	Ser	Ile	His	Pro	Glu	Ala	Phe	Ser	Thr	Leu	His	Ser	
125				360				365			370						

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128	Leu	Val	Lys	Leu	Asp	Leu	Thr	Asp	Asn	Gln	Leu	Thr	Thr	Leu	Pro	Leu	
129				375					380					385			
131	gct	gga	ctt	ggg	ggc	ttg	atg	cat	ctg	aag	ctc	aaa	ggg	aac	ctt	gct	1255
132	Ala	Gly	Leu	Gly	Gly	Leu	Met	His	Leu	Lys	Leu	Lys	Gly	Asn	Leu	Ala	
133				390					395					400			
135	ctc	tcc	cag	gcc	ttc	tcc	aag	gac	agt	ttc	cca	aaa	ctg	agg	atc	ctg	1303
136	Leu	Ser	Gln	Ala	Phe	Ser	Lys	Asp	Ser	Phe	Pro	Lys	Leu	Arg	Ile	Leu	
137				405					410					415			
139	gag	gtg	cct	tat	gcc	tac	cag	tgc	tgt	ccc	tat	ggg	atg	tgt	gcc	agc	1351
140	Glu	Val	Pro	Tyr	Ala	Tyr	Gln	Cys	Cys	Pro	Tyr	Gly	Met	Cys	Ala	Ser	
141	420						425					430				435	
143	ttc	ttc	aag	gcc	tct	ggg	cag	tgg	gag	gct	gaa	gac	ctt	cac	ctt	gat	1399
144	Phe	Phe	Lys	Ala	Ser	Gly	Gln	Trp	Glu	Ala	Glu	Asp	Leu	His	Leu	Asp	
145					440					445					450		
147	gat	gag	gag	tct	tca	aaa	agg	ccc	ctg	ggc	ctc	ctt	gcc	aga	caa	gca	1447
148	Asp	Glu	Glu	Ser	Ser	Lys	Arg	Pro	Leu	Gly	Leu	Leu	Ala	Arg	Gln	Ala	
149					455					460				465			
151	gag	aac	cac	tat	gac	cag	gac	ctg	gat	gag	ctc	cag	ctg	gag	atg	gag	1495
152	Glu	Asn	His	Tyr	Asp	Gln	Asp	Leu	Asp	Glu	Leu	Gln	Leu	Glu	Met	Glu	
153				470					475					480			
155	gac	tca	aag	cca	cac	ccc	agt	gtc	cag	tgt	agc	cct	act	cca	ggc	ccc	1543
156	Asp	Ser	Lys	Pro	His	Pro	Ser	Val	Gln	Cys	Ser	Pro	Thr	Pro	Gly	Pro	
157				485					490					495			
159	ttc	aag	ccc	tgt	gag	tac	ctc	ttt	gaa	agc	tgg	ggc	atc	cgc	ctg	gcc	1591
160	Phe	Lys	Pro	Cys	Glu	Tyr	Leu	Phe	Glu	Ser	Trp	Gly	Ile	Arg	Leu	Ala	
161	500					505					510					515	
163	gtg	tgg	gcc	atc	gtg	ttg	ctc	tcc	gtg	ctc	tgc	aat	gga	ctg	gtg	ctg	1639
164	Val	Trp	Ala	Ile	Val	Leu	Leu	Ser	Val	Leu	Cys	Asn	Gly	Leu	Val	Leu	
165					520						525				530		
167	ctg	acc	gtg	ttc	gct	ggc	ggg	cct	gtc	ccc	ctg	ccc	ccg	gtc	aag	ttt	1687
168	Leu	Thr	Val	Phe	Ala	Gly	Gly	Pro	Val	Pro	Leu	Pro	Pro	Val	Lys	Phe	
169				535						540				545			
171	gtg	gta	ggt	gcg	att	gca	ggc	gcc	aac	acc	ttg	act	ggc	att	tcc	tgt	1735
172	Val	Val	Gly	Ala	Ile	Ala	Gly	Ala	Asn	Thr	Leu	Thr	Gly	Ile	Ser	Cys	
173				550					555					560			
175	ggc	ctt	cta	gcc	tca	gtc	gat	gcc	ctg	acc	ttt	ggt	cag	ttc	tct	gag	1783
176	Gly	Leu	Leu	Ala	Ser	Val	Asp	Ala	Leu	Thr	Phe	Gly	Gln	Phe	Ser	Glu	
177				565					570					575			
179	tac	gga	gcc	cgc	tgg	gag	acg	ggg	cta	ggc	tgc	cgg	gcc	act	ggc	ttc	1831
180	Tyr	Gly	Ala	Arg	Trp	Glu	Thr	Gly	Leu	Gly	Cys	Arg	Ala	Thr	Gly	Phe	
181	580					585					590				595		
183	ctg	gca	gta	ctt	ggg	tgc	gag	gca	tgc	gtg	ctg	ctg	ctc	act	ctg	gcc	1879
184	Leu	Ala	Val	Leu	Gly	Ser	Glu	Ala	Ser	Val	Leu	Leu	Leu	Thr	Leu	Ala	
185					600						605				610		
187	gca	gtg	cag	tgc	agc	gtc	tcc	gtc	tcc	tgt	gtc	cgg	gcc	tat	ggg	aag	1927
188	Ala	Val	Gln	Cys	Ser	Val	Ser	Val	Ser	Cys	Val	Arg	Ala	Tyr	Gly	Lys	
189				615						620				625			
191	tcc	ccc	tcc	ctg	ggc	agc	gtt	cga	gca	ggg	gtc	cta	ggc	tgc	ctg	gca	1975

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196	Leu	Ala	Gly	Leu	Ala	Ala	Ala	Leu	Pro	Leu	Ala	Ser	Val	Gly	Glu	Tyr	
197		645					650				655						
199	ggg	gcc	tcc	cca	ctc	tgc	ctg	ccc	tac	gcg	cca	cct	gag	ggt	cag	cca	2071
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201	660					665					670					675	
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204	Ala	Ala	Leu	Gly	Phe	Thr	Val	Ala	Leu	Val	Met	Met	Asn	Ser	Phe	Cys	
205				680						685						690	
207	ttc	ctg	gtc	gtg	gcc	ggt	gcc	tac	atc	aaa	ctg	tac	tgt	gac	ctg	ccg	2167
208	Phe	Leu	Val	Ala	Gly	Ala	Tyr	Ile	Lys	Leu	Tyr	Cys	Asp	Leu	Pro		
209			695					700								705	
211	cgg	ggc	gac	ttt	gag	gcc	gtg	tgg	gac	tgc	gcc	atg	gtg	agg	cac	gtg	2215
212	Arg	Gly	Asp	Phe	Glu	Ala	Val	Trp	Asp	Cys	Ala	Met	Val	Arg	His	Val	
213			710					715								720	
215	gcc	tgg	ctc	atc	ttc	gca	gac	ggg	ctc	ctc	tac	tgt	ccc	gtg	gcc	ttc	2263
216	Ala	Trp	Leu	Ile	Phe	Ala	Asp	Gly	Leu	Leu	Tyr	Cys	Pro	Val	Ala	Phe	
217		725					730					735					
219	ctc	agc	ttt	gcc	tcc	atg	ctg	ggc	ctc	ttc	cct	gtc	acg	ccc	gag	gcc	2311
220	Leu	Ser	Phe	Ala	Ser	Met	Leu	Gly	Leu	Phe	Pro	Val	Thr	Pro	Glu	Ala	
221	740					745					750					755	
223	gtc	aag	tct	gtc	ctg	ctg	gtg	gtg	ctg	ccc	ctg	cct	gcc	tgc	ctc	aac	2359
224	Val	Lys	Ser	Val	Leu	Leu	Val	Val	Leu	Pro	Leu	Pro	Ala	Cys	Leu	Asn	
225				760						765						770	
227	cca	ctg	ctg	tac	ctg	ctc	ttc	aac	ccc	cac	ttc	cgg	gat	gac	ctt	cgg	2407
228	Pro	Leu	Leu	Tyr	Leu	Leu	Phe	Asn	Pro	His	Phe	Arg	Asp	Asp	Leu	Arg	
229			775					780								785	
231	cgg	ctt	cgg	ccc	cgc	gca	ggg	gac	tca	ggg	ccc	cta	gcc	tat	gct	gcg	2455
232	Arg	Leu	Arg	Pro	Arg	Ala	Gly	Asp	Ser	Gly	Pro	Leu	Ala	Tyr	Ala	Ala	
233			790					795								800	
235	gcc	ggg	gag	ctg	gag	aag	agc	tcc	tgt	gat	tct	acc	cag	gcc	ctg	gta	2503
236	Ala	Gly	Glu	Leu	Glu	Lys	Ser	Ser	Cys	Asp	Ser	Thr	Gln	Ala	Leu	Val	
237		805					810					815					
239	gcc	ttc	tct	gat	gtg	gat	ctc	att	ctg	gaa	gct	tct	gaa	gct	ggg	cgg	2551
240	Ala	Phe	Ser	Asp	Val	Asp	Leu	Ile	Leu	Glu	Ala	Ser	Glu	Ala	Gly	Arg	
241	820					825					830					835	
243	ccc	cct	ggg	ctg	gag	acc	tat	ggc	ttc	ccc	tca	gtg	acc	ctc	atc	tcc	2599
244	Pro	Pro	Gly	Leu	Glu	Thr	Tyr	Gly	Phe	Pro	Ser	Val	Thr	Leu	Ile	Ser	
245				840						845						850	
247	tgt	cag	cag	cca	ggg	gcc	ccc	agg	ctg	gag	ggc	agc	cat	tgt	gta	gag	2647
248	Cys	Gln	Gln	Pro	Gly	Ala	Pro	Arg	Leu	Glu	Gly	Ser	His	Cys	Val	Glu	
249			855					860								865	
251	cca	gag	ggg	aac	cac	ttt	ggg	aac	ccc	caa	ccc	tcc	atg	gat	gga	gaa	2695
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253			870					875								880	
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260 Gly Gly Gly Gly Phe Gln Pro Ser Gly Leu Ala Phe Ala Ser His Val
261 900      905      910      915
263 taaatatccc tccccattct tctcttcccc tctcttccct ttctctcttc cccctcggtg      2851
265 aatgatggct gcttctaaaa caaatacaac caaaactcag cagtgtgatc tatagcagga      2911
267 tggcccagtc cctggctcca ctgatcacct ctctcctgtg accatcacca acgggtgcct      2971
269 cttggcctgg ctttcccttg gccttcctca gcttcacctt gatactgggc ctcttccttg      3031
271 tcatgtctga agctgtggac cagagacctg gacttttgtc tgcttaaggg aaatgagggg      3091
273 agtaaagaca gtgaaggggt ggaggggtga tcagggcaca gtggacaggg agacctcaca      3151
275 gagaaaggcc tggaagggtga tttcccggtg gactcatgga taggatacaa aatgtgttcc      3211
277 atgtaccatt aatcttgaca tatgccatgc ataaagactt cctattaaaa taagctttgg      3271
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284 <212> TYPE: PRT
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293 Ser Ala Arg Asp Leu Ser Met Asn Asn Leu Thr Glu Leu Gln Pro Gly
294      20      25      30
297 Leu Phe His His Leu Arg Phe Leu Glu Glu Leu Arg Leu Ser Gly Asn
298      35      40      45
301 His Leu Ser His Ile Pro Gly Gln Ala Phe Ser Gly Leu Tyr Ser Leu
302      50      55      60
305 Lys Ile Leu Met Leu Gln Asn Asn Gln Leu Gly Gly Ile Pro Ala Glu
306 65      70      75      80
309 Ala Leu Trp Glu Leu Pro Ser Leu Gln Ser Leu Arg Leu Asp Ala Asn
310      85      90      95
313 Leu Ile Ser Leu Val Pro Glu Arg Ser Phe Glu Gly Leu Ser Ser Leu
314      100      105      110
317 Arg His Leu Trp Leu Asp Asp Asn Ala Leu Thr Glu Ile Pro Val Arg
318      115      120      125
321 Ala Leu Asn Asn Leu Pro Ala Leu Gln Ala Met Thr Leu Ala Leu Asn
322      130      135      140
325 Arg Ile Ser His Ile Pro Asp Tyr Ala Phe Gln Asn Leu Thr Ser Leu
326 145      150      155      160
329 Val Val Leu His Leu His Asn Asn Arg Ile Gln His Leu Gly Thr His
330      165      170      175
333 Ser Phe Glu Gly Leu His Asn Leu Glu Thr Leu Asp Leu Asn Tyr Asn
334      180      185      190
337 Lys Leu Gln Glu Phe Pro Val Ala Ile Arg Thr Leu Gly Arg Leu Gln
338      195      200      205
341 Glu Leu Gly Phe His Asn Asn Asn Ile Lys Ala Ile Pro Glu Lys Ala
342      210      215      220
345 Phe Met Gly Asn Pro Leu Gln Thr Ile His Phe Tyr Asp Asn Pro
346 225      230      235      240
349 Ile Gln Phe Val Gly Arg Ser Ala Phe Gln Tyr Leu Pro Lys Leu His

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Input Set : A:\Sequence\_Listing.txt

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
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L:531 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:529  
L:775 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:773  
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